What is claimed is:

1. A method of determining an expression pattern of one or more families of transposable elements in a sample comprising determining expression of one or more families of transposable elements.

2. A method of assigning an expression pattern of transposable elements to a type of cancerous cell in a sample, comprising:
   a) determining expression of one or more families of transposable elements; and
   b) assigning the expression pattern obtained from step a) to the type of cancerous cell in the sample.

3. The method of claim 2, wherein the expression pattern is determined by microarray analysis.

4. The method of claim 2, wherein the sample comprises a cell selected from the group consisting of: a carcinoma cell, a fibroma cell, a carcinoma cell, a sarcoma cell, a teratoma cell, and a blastoma cell.

5. The method of claim 2, wherein the sample comprises mixed cell types from a tumor.

6. The method of claim 2, wherein the sample comprises a breast tumor cell of epithelial origin.

7. The method of claim 2, wherein the sample comprises an ovarian tumor cell of epithelial, stromal or germ cell origin.

8. The method of any of claims 1-7, wherein the transposable elements are retroelements.

9. A method of diagnosing cancer comprising:
    a) determining expression of one or more families of transposable elements in a sample to obtain an expression pattern;
    b) matching the expression pattern of step a) with a known expression pattern for a type of cancer; and
    c) diagnosing the type of cancer based on matching of the expression pattern of with a known expression pattern for a type of cancer.

10. The method of any of claims 1- 9, wherein the expression pattern is determined by
microarray analysis.

11. The method of claim 9, wherein one or more of the families of transposable elements is selected from the group consisting of retroelement families and DNA element families.

12. The method of claim 11, wherein one or more of the families of retroelements is selected from the group consisting of a family of endogenous retroviruses (ERVs), a family of short interspersed nuclear elements (SINES) and a family of long interspersed nuclear elements (LINEs).

13. A method of determining the effectiveness of an anti-cancer therapeutic in a subject comprising:
    a) determining expression of one or more families of transposable elements, in a sample obtained from the subject, to obtain a first expression pattern;
    b) administering an anti-cancer therapeutic to the subject;
    c) determining expression of one or more families of transposable elements in a sample obtained from the subject after administration of an anti-cancer therapeutic to obtain a second expression pattern; and

d) comparing the second expression pattern with the first expression pattern such that if fewer transposable elements are differentially expressed in the second expression pattern as compared to the first expression pattern, the anti-cancer therapeutic is an effective anti-cancer therapeutic.

14. The method of any of claims 1-13, wherein expression of the transposable elements is measured by assaying for the mRNA transcribed from the genes or proteins translated from an mRNA transcribed from the genes.

15. The method of any of claims 1-13, wherein expression of two or more families of transposable elements is determined and used to form the pattern of expression.

16. A method of determining a methylation pattern of one or more families of transposable elements in a sample comprising determining methylation of one or more families of transposable elements.

17. A method of assigning a methylation pattern of transposable elements to a type of cancerous cell in a sample, comprising:

a) determining methylation of one or more families of transposable elements; and

b) assigning the methylation pattern obtained from step a) to the type of cancerous cell in the sample.

18. The method of claim 17, wherein the sample comprises a cell selected from the group consisting of: a carcinoma cell, a fibroma cell, a carcinoma cell, a sarcoma cell, a teratoma cell, and a blastoma cell.

19. The method of claim 17, wherein the sample comprises mixed cell types from a tumor.

20. The method of claim 17, wherein the sample comprises a breast tumor cell of epithelial origin.

21. The method of claim 17, wherein the sample comprises an ovarian tumor cell of epithelial, stromal or germ cell origin.

22. The method of any of claims 17-21, wherein the transposable elements are selected from the group consisting of retroelements and DNA elements.

23. A method of diagnosing cancer comprising:
    a) determining methylation of one or more families of transposable elements in a sample to obtain a methylation pattern;
    b) comparing the methylation pattern of step a) with a known methylation pattern for a type of cancer; and
    c) diagnosing the type of cancer based on matching of the methylation pattern of a) with a known methylation pattern for a type of cancer.

24. A method of determining the effectiveness of an anti-cancer therapeutic in a subject comprising:
    a) determining methylation of one or more families of transposable elements, in a sample obtained from the subject, to obtain a first methylation pattern;
    b) administering an anti-cancer therapeutic to the subject;
    c) determining methylation of one or more families of transposable elements in a sample obtained from the subject after administration of an anti-cancer therapeutic to obtain a second methylation pattern; and
    d) comparing the second methylation pattern with the first methylation pattern such that if there is a change in the second methylation pattern as compared to the first

methylation pattern, the anti-cancer therapeutic is an effective anti-cancer therapeutic.

25. The method of any of claims 16-24, wherein methylation of the transposable element genes is measured by contacting the methylated transposable element gene sequence with an antibody that specifically binds a methylated sequence.

26. The method of any of claims 16-24, wherein methylation of the transposable element genes is measured by contacting the methylated transposable element gene sequence with an antibody that specifically binds a methylation complex protein associated with the methylated transposable element gene sequence.

27. The method of any of claims 16-24, wherein methylation of the transposable element genes is monitored by enzymatic means.

28. The method of any of claims 16-24, wherein methylation of the transposable element genes is monitored by microarray analysis.

29. The method of any of claims 16-24, wherein methylation of the transposable element genes is monitored by methylation-specific PCR.

30. The method of any of claims 16-24, wherein the methylation of two or more families of transposable elements is determined and used to form the methylation pattern.

31. A method of determining a chromatin status pattern of one or more families of transposable elements in a sample comprising determining chromatin status of one or more families of transposable elements.

32. A method of assigning a chromatin status pattern of transposable elements to a type of cancerous cell in a sample, comprising:

a) determining chromatin status of one or more families of transposable elements; and

b) assigning the chromatin status pattern obtained from step a) to the type of cancerous cell in the sample.

33. The method of claim 32, wherein the sample comprises a cell selected from the group consisting of: a carcinoma cell, a fibroma cell, a carcinoma cell, a sarcoma cell, a teratoma cell, and a blastoma cell.

34. The method of claim 32, wherein the sample comprises mixed cell types from a tumor.

35. The method of claim 32, wherein the sample comprises a breast tumor cell of epithelial origin.

36. The method of claim 32, wherein the sample comprises an ovarian tumor cell of epithelial, stromal or germ cell origin.

37. The method of any of claims 31-36, wherein the transposable elements are selected from the group consiting of retroelements and DNA elements.

38. A method of diagnosing cancer comprising:

a) determining the chromatin status of one or more families of transposable elements in a sample to obtain a chromatin status pattern;

b) comparing the chromatin status pattern of step a) with a known chromatin status pattern for a type of cancer; and

c) diagnosing the type of cancer based on matching of the chromatin status pattern of a with a known chromatin status pattern for a type of cancer.

39. A method of determining the effectiveness of an anti-cancer therapeutic in a subject comprising:

a) determining the chromatin status of one or more families of transposable elements, in a sample obtained from the subject, to obtain a first chromatin status pattern;

b) administering an anti-cancer therapeutic to the subject;

c) determining chromatin status of one or more families of transposable elements in a sample obtained from the subject after administration of an anti-cancer therapeutic to obtain a second chromatin status pattern; and

d) comparing the second chromatin status pattern with the first chromatin status pattern such that if there is a change in the second chromatin status pattern as compared to the first chromatin status pattern, the anti-cancer therapeutic is an effective anti-cancer therapeutic.

40. The method of any of claims 31-39, wherein chromatin status of the transposable element genes is measured by determining the accessibility of transposable element genes to a restriction enzyme.

41. The method of any of claims 31-40, wherein chromatin status of the transposable element genes is monitored by microarray analysis.

42. The method of any of claims 16-24, wherein the chromatin status of two or more families of transposable elements is determined and used to form the chromatin status pattern.